

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Ashkenazi, Avi J.

(ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES

(iii) NUMBER OF SEQUENCES: 11

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 460 Point San Bruno Blvd

(C) CITY: South San Francisco

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(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 31-Mar-1997

(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Marschang, Diane L.

(B) REGISTRATION NUMBER: 35,600

(C) REFERENCE/DOCKET NUMBER: P1007R1

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415/225-5416

(B) TELEFAX: 415/952-9881

(C) TELEX: 910/371-7168

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: Amino Acid

10 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

15 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15
20 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 25 30
25 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
35 40 45
Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60
25 Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
65 70 75
30 Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
80 85 90
Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
95 100 105
35 Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly

110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro

125 130 135

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Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His

140 145 150

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Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys

155 160 165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro

170 175 180

15

Thr

181

(2) INFORMATION FOR SEQ ID NO:2:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 433 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50

30

TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTGC AGAGGCTGCC 100

CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150

35

ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200

TAATTCTGAA TGTGCCCCGT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
 TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
 5 CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350
 CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
 ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28

(2) INFORMATION FOR SEQ ID NO:4:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

35 CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1438 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
AGCTCTATCC TGTGCCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCGCCTCC 250
CCCCGCCCCG CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
AGATTGGTCT GTTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550
GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600

AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCCTG 650
 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
 5 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
 10 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950
 15 GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
 GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
 20 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTC 1150
 CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200
 25 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300
 ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
 30 AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
 TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438

35 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 417 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
1 5 10 15

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 25 30

Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
15 35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60

Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
20 65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
25 80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
30 110 115 120

Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
125 130 135

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
35

		140		145		150
	Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys					
		155		160		165
5	Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro					
		170		175		180
	Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys					
10		185		190		195
	Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu					
		200		205		210
15	Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg					
		215		220		225
	His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly					
		230		235		240
20	Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu					
		245		250		255
	Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys					
25		260		265		270
	Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr					
		275		280		285
30	Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp					
		290		295		300
	Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr					
		305		310		315
35						

Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln
 320 325 330

Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg
 335 340 345

Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu
 350 355 360

Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln
 365 370 375

Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu
 380 385 390

Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
 395 400 405

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
 410 415 417

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10 TTCGGCCGAG AAGTTGAGAA ATGTC 25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1634 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50

ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94
Met Glu

1

CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu

5

10

15

CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr

20

25

CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
 30 35 40

5 AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
 45 50

10 CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
 His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
 55 60 65

15 TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328
 Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
 70 75 80

20 TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367
 Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln
 85 90

25 GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406
 Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn
 95 100 105

30 TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445
 Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro
 110 115

35 GGC TGG TTT GTG GAG TGC CAG GTC AGC CAA TGT GTC AGC 484
 Gly Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser
 120 125 130

AGT TCA CCC TTC TAC TGC CAA CCA TGC CTA GAC TGC GGG 523
 Ser Ser Pro Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly
 135 140 145

	GCC	CTG	CAC	CGC	CAC	ACA	CGG	CTA	CTC	TGT	TCC	CGC	AGA	562
	Ala	Leu	His	Arg	His	Thr	Arg	Leu	Leu	Cys	Ser	Arg	Arg	
					150					155				
5	GAT	ACT	GAC	TGT	GGG	ACC	TGC	CTG	CCT	GGC	TTC	TAT	GAA	601
	Asp	Thr	Asp	Cys	Gly	Thr	Cys	Leu	Pro	Gly	Phe	Tyr	Glu	
		160					165					170		
	CAT	GGC	GAT	GGC	TGC	GTG	TCC	TGC	CCC	ACG	AGC	ACC	CTG	640
10	His	Gly	Asp	Gly	Cys	Val	Ser	Cys	Pro	Thr	Ser	Thr	Leu	
				175					180					
	GGG	AGC	TGT	CCA	GAG	CGC	TGT	GCC	GCT	GTC	TGT	GGC	TGG	679
	Gly	Ser	Cys	Pro	Glu	Arg	Cys	Ala	Ala	Val	Cys	Gly	Trp	
15		185				190					195			
	AGG	CAG	ATG	TTC	TGG	GTC	CAG	GTG	CTC	CTG	GCT	GGC	CTT	718
	Arg	Gln	Met	Phe	Trp	Val	Gln	Val	Leu	Leu	Ala	Gly	Leu	
			200					205					210	
20	GTG	GTC	CCC	CTC	CTG	CTT	GGG	GCC	ACC	CTG	ACC	TAC	ACA	757
	Val	Val	Pro	Leu	Leu	Leu	Gly	Ala	Thr	Leu	Thr	Tyr	Thr	
					215					220				
25	TAC	CGC	CAC	TGC	TGG	CCT	CAC	AAG	CCC	CTG	GTT	ACT	GCA	796
	Tyr	Arg	His	Cys	Trp	Pro	His	Lys	Pro	Leu	Val	Thr	Ala	
			225					230				235		
	GAT	GAA	GCT	GGG	ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	835
30	Asp	Glu	Ala	Gly	Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	
				240					245					
	ACC	CAT	CTG	TCA	CCC	TTG	GAC	AGC	GCC	CAC	ACC	CTT	CTA	874
	Thr	His	Leu	Ser	Pro	Leu	Asp	Ser	Ala	His	Thr	Leu	Leu	
35		250					255					260		

	GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG	913
	Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln	
	265 270 275	
5	TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC	952
	Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr	
	280 285	
10	CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC	991
	Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp	
	290 295 300	
15	CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC	1030
	Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro	
	305 310	
20	ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG	1069
	Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met	
	315 320 325	
25	ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC	1108
	Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp	
	330 335 340	
30	GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG	1147
	Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr	
	345 350	
35	CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG	1186
	Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val	
	355 360 365	
35	GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC	1225
	Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu	
	370 375	

AAG CGC TGG CGC CAG CAG CAG CCC GCG GGC CTC GGA GCC 1264
Lys Arg Trp Arg Gln Gln Gln Pro Ala Gly Leu Gly Ala
380 385 390

5 GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303
Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
395 400 405

10 GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340
Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
410 415 417

GACACGGCGC CCACTTGCCA CCTAGGCGCT CTGGTGGCCC TTGCAGAAGC 1390

15 CCTAAGTACG GTTACTTATG CGTGTAGACA TTTTATGTCA CTTATTAAGC 1440

CGCTGGCACG GCCCTGCGTA GCAGCACCAG CCGGCCCCAC CCCTGCTCGC 1490

20 CCCTATCGCT CCAGCCAAGG CGAAGAAGCA CGAACGAATG TCGAGAGGGG 1540

GTGAAGACAT TTCTCAACTT CTCGGCCGGA GTTTGGCTGA GATCGCGGTA 1590

TTAAATCTGT GAAAGAAAAC AAAAAAAAAA AAAAAAAAAA AAAA 1634

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: Nucleic Acid

30 (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

(2) INFORMATION FOR SEQ ID NO:11:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30

15
A
G
G
A
T
G
G
G
A
A
G
T
G
T
G
T
G
A
T
A
T
A
T
C
C
T
T
G
A
T